

REMARKS

Claim 1 was objected to due to a noted informality. The claim has been amended in the manner suggest by the Examiner.

Claims 1, 3-8 and 13-17 were rejected under 35 U.S.C. 112, second paragraph, as being indefinite. The Examiner objects to use of the term “likely” as being an impermissible relative term. Claims 1, 13 and 15-17 have been amended to address this issue. With respect to claim 5, the Examiner has identified an number of antecedent issues. Amendments are presented to claim 5 to address the noted issues. With respect to claim 8, the Examiner has identified antecedent issues. Amendments are presented to claim 8 to address the noted issues. Withdrawal of the Section 112 rejection is requested.

Claims 1, 3-8 and 13-17 were rejected under 35 U.S.C. 103(a) as being unpatentable over Getz in view of Dougherty and Tolley. Claim 1 recites “identifying in sub-tables groups of genes that satisfy said clustering criterion” and “generating a corresponding filtered sub-table containing data of genes having expression values which satisfy said logic filtering criterion” and “establishing pair combinations of said sub-tables.” Thus, claim 1 requires filtered sub-tables, wherein each sub-table includes genes which have satisfied certain logic filtering criteria. Claim 1 still further requires that *plural pair combinations of sub-tables* be established (i.e., combined pairs of gene sub-tables). The Examiner asserts that this is taught by Getz. Applicants respectfully disagree.

With reference to Getz page 12079, left column, Getz summarizes the disclosed “philosophy.” Getz states that “We look for pairs of a relatively small subset F_i of features (either genes or samples) and of objects O_j , (samples or genes), such that when the objects in O_j are represented using only the features from F_i , clustering yields stable and significant partitions.” Applicants submit that this teaching of Getz relates to the distinct formation of a subset of genes (g) and a subset of samples (s). This teaching, by itself, fails to reach all of the claim limitations concerning the *sub-tables and pair combinations of sub-tables*. The reason for this is that Applicants specifically claim “establishing pair combinations of said sub-tables.” By this it is meant pairs of sub-tables in combination, wherein each of the included sub-tables in the

pair combination “contain[s] data of genes having expression values which satisfy said logic filtering criterion.” This would be combined pairs of gene sub-tables. Getz, through his pairing operation associates (or pairs) features or objects. Thus, Getz’s pairs include, for example, clustered genes, which are analogous to Applicants’ sub-tables. Getz does not go the additional step recited by Applicants in claim 1 of pairing (gene) sub-tables in a *pair combination*. Getz fails to teach or suggest combining in pairs different clusters (sub-tables) of genes.

The Examiner points to Getz page 12080 in support of the rejection. Applicants respectfully disagree with the Examiner’s technical analysis. Getz teaches on page 12080 distinctly forming a stable subset of samples and a stable subset of genes. A pair is created from the combination of a sample subset (s) and a gene subset (g). This would be a sample/gene pair combination. This is not a teaching, however, of the claimed invention which “establish[es] pair combinations of said sub-tables” wherein each sub-table “contain[s] data of genes having expression values which satisfy said logic filtering criterion.” Pairing in Getz always involves a sample subset (s) and a gene subset (g), and never, as is claimed by Applicants, pairs of gene sub-tables.

Applicants further note that Getz teaches the performance of an iterative clustering process. For example, the abstract recites “an algorithm, based on iterative clustering.” Further, page 12080, left column, paragraph 2, states with respect to clustering that “These steps are iterated further” This iterative process disclosed in Getz for clustering is quite different from the claimed process recited in claim 1 which the clustering process is performed just once on the data. No iterative clustering operation is performed. Once the sub-tables are formed by clustering, as claimed, the process moves on to the formation of pair combinations of sub-tables. This is distinct from Getz which teaches starting from a parent pair (g, s), and then iteratively progressing from the parent to additional pairs (g, s) until no new clusters are found.

Claim 1 further recites “generating for each pair combination a characteristic value” and “identifying the groups of genes associated with pair combinations whose characteristic value is greater than a certain pre-established threshold as being members of a network of genes.” Applicants respectfully submit that Getz does not teach an operation to identify a group of genes “as being members of a network of genes.” Rather, as taught by Getz on page 12080 (left

column), applications of the Getz process allow for a) the “identif[ication of] genes that partition the samples according to a certain known classification of samples,” b) the “discover[y of] new partitions,” c) the “identif[ication of] subpartitions,” and d) the revelation of “conditional correlations among genes.” As recognized by those skilled in the art, none of these “applications” of the Getz process teaches “identifying the groups of genes associated with pair combinations ... as being *members of a network of genes*.”

Applicants further point out that claim 1 also requires a certain threshold examination be performed. Claim 1 recites “generating for each pair combination a characteristic value” and “identifying the groups of genes associated with pair combinations *whose characteristic value is greater than a certain pre-established threshold* as being members of a network of genes.” The Examiner points to the temperature threshold analysis described in Getz in the paragraph bridging pages 12080 and 12081. This temperature analysis, however, is related to the clustering process (SPC is a hierarchical clustering method), and not to any process for taking a characteristic value of a pair combination (gene sub-tables) and comparing that value against a threshold for determining membership in a network of genes as claimed by Applicants. This temperature teaching in the context of SPC clustering is simply irrelevant to the claimed limitations for identifying members within a network of genes. The determination as to whether a stable cluster has been reached in Getz through temperature testing does not teach or suggest threshold analysis with respect to characteristic values of pair combinations of (gene) sub-tables and gene network membership.

In view of the foregoing, Applicants submit that claim 1 distinguishes over the cited prior art and is in condition for allowance. Applicants further request rejoinder of dependent claims 9-12.

Claim 13 recites “generating sub-tables of data in groups of genes that satisfy a pre-established clustering criterion” and “considering all possible pairs of generated sub-tables” wherein those sub-tables relate to groups of genes. As discussed above, Getz fails to teach or suggest pairing gene sub-tables. At best, Getz teaches a pairing of a sample subset (s) and a gene subset (g), and not paired gene sub-tables as claimed. In view of the foregoing, Applicants submit that claim 13 distinguishes over the cited prior art and is in condition for allowance.

Applicants further claim in claim 13 “generating for each pair of sub-tables a characteristic value determined as a function of the characteristic parameters and outputting data identifying groups of genes from each pair of sub-tables whose characteristic value is greater than a certain pre-established threshold as being members of a network of genes.” For at least the reasons discussed above in connection with claim 1, Applicants submit that Getz fails to teach or suggest these claim limitations.

In claim 15, the limitations are “identify clusters in the form of sub-tables comprising groups of genes that satisfy certain clustering criterion” and “establishing all possible pair combinations of said clusters.” Again, Getz fails to teach or suggest pairing gene clusters (sub-tables). At best, Getz teaches a pairing of a sample subset (s) and a gene subset (g), and not paired gene sub-tables as claimed. In view of the foregoing, Applicants submit that claim 15 distinguishes over the cited prior art and is in condition for allowance.

Applicants further claim in claim 15 “calculating a characteristic value for the cluster pair” and “identifying the genes associated with cluster pair combinations whose characteristic value is greater than a certain pre-established threshold as being members of a network of genes.” For at least the reasons discussed above in connection with claim 1, Applicants submit that Getz fails to teach or suggest these claim limitations.

Claim 16 recites forming “sub-tables comprising groups of genes that satisfy certain filtering criteria” and “establishing all possible pair combinations of said clusters.” As discussed above, Getz fails to teach or suggest pairing gene sub-tables. At best, Getz teaches a pairing of a sample subset (s) and a gene subset (g), and not paired gene sub-tables as claimed. In view of the foregoing, Applicants submit that claim 16 distinguishes over the cited prior art and is in condition for allowance.

Applicants further claim in claim 16 “calculating a characteristic value for the pair combination” and “identifying the genes associated with pair combinations whose characteristic value is greater than a certain pre-established threshold as being members of a network of genes.” For at least the reasons discussed above in connection with claim 1, Applicants submit that Getz fails to teach or suggest these claim limitations.

Claim 16 further recites “establishing all possible pair combinations of said clusters, all possible pair combinations of filter data, and all possible pair combinations of clusters and filter data” The distinction with respect to Getz and concerning pair combinations of clusters (genes) is discussed above. With respect to the remaining claimed pair combinations, Applicants submit that Getz also fails to teach or suggest “pair combinations of filter data” or “pair combinations of clusters and filter data.” Notably, the Examiner’s analysis on page 5 of the office action ignores the “pair combinations of filter data” or “pair combinations of clusters and filter data” limitations of claim 16. Applicants respectfully request that the Examiner specifically identify how Gets meets these claim limitations, or withdraw the rejection.

Claim 17 includes limitations similar to claim 13. For at least the reasons recited above in connection with claim 13, claim 17 is patentable over the cited prior art.

In view of the foregoing, Applicants respectfully submit that the application is in condition for favorable action and allowance.

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Respectfully submitted,

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